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In re International Patent Application of

DUKE UNIVERSITY ET AL

Agent's File Ref: **1579-379**

International Application No: **PCT/US99/17678**
International Filing Date: 05 August 1999

For: URATE OXIDASE

19 November 1999

United States Receiving Office
Honorable Commissioner of Patents
and Trademarks
Washington, D.C. 20231

Response to Correct Defects in International Application

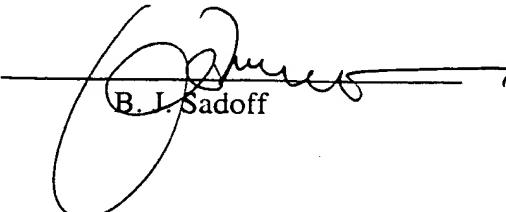
Dear Sirs,

Attached is a printed sequence listing for this application and a copy of the computer readable form on a 3.5" disk in the attached envelope.

In accordance with 37 CFR 1.821-1.825, I hereby state that the content of the paper and computer-readable copies of the sequence listing submitted in accordance with 37 CFR 1.821(c) and (e), respectively, are the same. I hereby state that the submission, filed in accordance with 37 CFR 1.821(g), does not introduce new matter.

Respectfully submitted,

NIXON & VANDERHYE P.C.



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SEQUENCE LISTING

<110> HERSHFIELD, MICHAEL S.
KELLY, SUSAN J.

<120> URATE OXIDASE

<130> 1579-379

<140> PCT/US99/17678
<141> 1999-08-05

<160>11

<170> PatentIn Ver. 2.0

<210> 1
<211> 915

<212> DNA

<213> Artificial Sequence

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<221> CDS

<222> (1)...(915)

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<223> Description of Artificial Sequence:PBC CHIMERA

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gtc cga act ggc tat ggg aag gat atg ata aaa gtt ctc cat att cag	96
Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln	
20 25 30	
cga gat gga aaa tat cac agc att aaa gag gtg gca act tca gtg caa	144
Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln	
35 40 45	
ctg act ttg agc tcc aaa aaa gat tac ctg cat gga gac aat tca gat	192
Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp	
50 55 60	
gtc atc cct aca gac acc atc aag aac aca gtt aat gtc ctg gcg aag	240
Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys	
65 70 75 80	
tcc aaa ggc atc aaa agc ata gaa act ttt gct gtg act atc tgt gag	288
Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu	
85 90 95	
cat ttc ctt tct tcc ttc aag cat gtc atc aga gct caa gtc tat gtg	336
His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val	
100 105 110	
gaa gaa gtt cct tgg aag cgt ttt gaa aag aat gga gtt aag cat gtc	384
Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val	
115 120 125	
cat gca ttt att tat act cct act gga acg cac ttc tgt gag gtt gaa	432
His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu	
130 135 140	

cag ata agg aat gga cct cca gtc att cat tct gga atc aaa gac cta	480
Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu	
145 150 155 160	
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Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp	
165 170 175	
cag ttc acc acc ctc cct gag gtg aag gac cgg tgc ttt gcc acc caa	576
Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln	
180 185 190	
gtg tac tgc aaa tgg cgc tac cac cag ggc aga gat gtg gac ttt gag	624
Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu	
195 200 205	
gcc acc tgg gac act gtt agg agc att gtc ctg cag aaa ttt gct ggg	672
Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly	
210 215 220	
ccc tat gac aaa ggc gag tac tca ccc tct gtg cág aag acc ctc tat	720
Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr	
225 230 235 240	
gat atc cag gtg ctc tcc ctg agc cga gtt cct gag ata gaa gat atg	768
Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met	
245 250 255	
gaa atc agc ctg cca aac att cac tac ttc aat ata gac atg tcc aaa	816
Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys	
260 265 270	
atg ggt ctg atc aac aag gaa gag gtc ttg ctg cca tta gac aat cca	864
Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro	
275 280 285	
tat gga aaa att act ggt aca gtc aag agg aag ttg tct tca aga ctg	912
Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu	
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tga	915
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20 25 30	
Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln	
35 40 45	
Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp	
50 55 60	
Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys	
65 70 75 80	

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
 85 90 95
 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
 100 105 110
 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
 115 120 125
 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
 130 135 140
 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
 145 150 155 160
 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
 165 170 175
 Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
 180 185 190
 Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
 195 200 205
 Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
 210 215 220
 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
 225 230 235 240
 Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met
 245 250 255
 Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys
 260 265 270
 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
 275 280 285
 Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
 290 295 300

<210> 3
 <211> 915
 <212> DNA
 <213> Artificial Sequence

<220>
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 <222> (1)...(915)

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gtc cga act ggc tat ggg aag gat atg ata aaa gtt ctc cat att cag 96
 Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
 20 25 30

cga gat gga aaa tat cac agc att aaa gag gtg gca act tca gtg caa	144
Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln	
35	40
45	
ctg act ttg agc tcc aaa aaa gat tac ctg cat gga gac aat tca gat	192
Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp	
50	55
60	
gtc atc cct aca gac acc atc aag aac aca gtt aat gtc ctg gcg aag	240
Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys	
65	70
75	80
tcc aaa ggc atc aaa agc ata gaa act ttt gct gtg act atc tgt gag	288
Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu	
85	90
95	
cat ttc ctt tct tcc ttc aag cat gtc atc aga gct caa gtc tat gtg	336
His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val	
100	105
110	
gaa gaa gtt cct tgg aag cgt ttt gaa aag aat gga gtt aag cat gtc	384
Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val	
115	120
125	
cat gca ttt att tat act cct act gga acg cac ttc tgt gag gtt gaa	432
His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu	
130	135
140	
cag ata agg aat gga cct cca gtc att cat tct gga atc aaa gac cta	480
Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu	
145	150
155	160
aaa gtc ttg aaa aca acc cag tct ggc ttt gaa gga ttc atc aag gac	528
Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp	
165	170
175	
cag ttc acc acc ctc cct gag gtg aag gac cgg tgc ttt gcc acc caa	576
Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln	
180	185
190	
gtg tac tgc aaa tgg cgc tac cac cag ggc aga gat gtg gac ttt gag	624
Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu	
195	200
205	
gcc acc tgg gac act gtt agg agc att gtc ctg cag aaa ttt gct ggg	672
Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly	
210	215
220	
ccc tat gac aaa ggc gag tac tcg ccc tct gtc cag aag aca ctc tat	720
Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr	
225	230
235	240
gac atc cag gtg ctc acc ctg ggc cag gtt cct gag ata gaa gat atg	768
Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met	
245	250
255	
gaa atc agc ctg cca aat att cac tac tta aac ata gac atg tcc aaa	816
Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys	
260	265
270	
atg gga ctg atc aac aag gaa gag gtc ttg cta cct tta gac aat cca	864
Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro	
275	280
285	

tat gga aaa att act ggt aca gtc aag agg aag ttg tct tca aga ctg 912
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tga 915

305

<210> 4
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 <212> PRT
 <213> Artificial Sequence

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 20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
 35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
 50 55 60

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
 65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
 85 90 95

His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
 100 105 110

Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
 115 120 125

His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
 130 135 140

Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
 145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
 165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
 180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
 195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
 210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
 225 230 235 240

Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met
 245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys
 260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
 275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
 290 295 300

<210> 5

<211> 304

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:baboon D3H

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 20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
 35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
 50 55 60

Ile Ile Pro Thr Asp Thr Ile Lys Asn Thr Val His Val Leu Ala Lys
 65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Ala Phe Gly Val Asn Ile Cys Glu
 85 90 95

Tyr Phe Leu Ser Ser Phe Asn His Val Ile Arg Ala Gln Val Tyr Val
 100 105 110

Glu Glu Ile Pro Trp Lys Arg Leu Glu Lys Asn Gly Val Lys His Val
 115 120 125

His Ala Phe Ile His Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
 130 135 140

Gln Leu Arg Ser Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
 145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
 165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
 180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Cys Arg Asp Val Asp Phe Glu
 195 200 205

Ala Thr Trp Gly Thr Ile Arg Asp Leu Val^f Leu Glu Lys Phe Ala Gly
 210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
 225 230 235 240

Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met
 245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys
 260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
 275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
 290 295 300

<210> 6
 <211> 304
 <212> PRT
 <213> baboon

<400> 6
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 20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
 35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
 50 55 60

Ile Ile Pro Thr Asp Thr Ile Lys Asn Thr Val His Val Leu Ala Lys
 65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Ala Phe Gly Val Asn Ile Cys Glu
 85 90 95

Tyr Phe Leu Ser Ser Phe Asn His Val Ile Arg Ala Gln Val Tyr Val
 100 105 110

Glu Glu Ile Pro Trp Lys Arg Leu Glu Lys Asn Gly Val Lys His Val
 115 120 125

His Ala Phe Ile His Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
 130 135 140

Gln Leu Arg Ser Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
 145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
 165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
 180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Cys Arg Asp Val Asp Phe Glu
 195 200 205

Ala Thr Trp Gly Thr Ile Arg Asp Leu Val Leu Glu Lys Phe Ala Gly
 210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
 225 230 235 240

Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met
 245 250 255

Glu	Ile	Ser	Leu	Pro	Asn	Ile	His	Tyr	Phe	Asn	Ile	Asp	Met	Ser	Lys
260															
Met	Gly	Leu	Ile	Asn	Lys	Glu	Glu	Val	Leu	Leu	Pro	Leu	Asp	Asn	Pro
275															
Tyr	Gly	Lys	Ile	Thr	Gly	Thr	Val	Lys	Arg	Lys	Leu	Ser	Ser	Arg	Leu
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295															300

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 <212> PRT
 <213> pig

<400> 7															
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Val	Arg	Thr	Gly	Tyr	Gly	Lys	Asp	Met	Ile	Lys	Val	Leu	His	Ile	Gln
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Arg	Asp	Gly	Lys	Tyr	His	Ser	Ile	Lys	Glu	Val	Ala	Thr	Ser	Val	Gln
								35	40						45
Leu	Thr	Leu	Ser	Ser	Lys	Lys	Asp	Tyr	Leu	His	Gly	Asp	Asn	Ser	Asp
								50	55						60
Val	Ile	Pro	Thr	Asp	Thr	Ile	Lys	Asn	Thr	Val	Asn	Val	Leu	Ala	Lys
								65	70						80
Phe	Lys	Gly	Ile	Lys	Ser	Ile	Glu	Thr	Phe	Ala	Val	Thr	Ile	Cys	Glu
								85	90						95
His	Phe	Leu	Ser	Ser	Phe	Lys	His	Val	Ile	Arg	Ala	Gln	Val	Tyr	Val
								100	105						110
Glu	Glu	Val	Pro	Trp	Lys	Arg	Phe	Glu	Lys	Asn	Gly	Val	Lys	His	Val
								115	120						125
His	Ala	Phe	Ile	Tyr	Thr	Pro	Thr	Gly	Thr	His	Phe	Cys	Glu	Val	Glu
								130	135						140
Gln	Ile	Arg	Asn	Gly	Pro	Pro	Val	Ile	His	Ser	Gly	Ile	Lys	Asp	Leu
								145	150						160
Lys	Val	Leu	Lys	Thr	Thr	Gln	Ser	Gly	Phe	Glu	Gly	Phe	Ile	Lys	Asp
								165	170						175
Gln	Phe	Thr	Thr	Leu	Pro	Glu	Val	Lys	Asp	Arg	Cys	Phe	Ala	Thr	Gln
								180	185						190
Val	Tyr	Cys	Lys	Trp	Arg	Tyr	His	Gln	Gly	Arg	Asp	Val	Asp	Phe	Glu
								195	200						205
Ala	Thr	Trp	Asp	Thr	Val	Arg	Ser	Ile	Val	Leu	Gln	Lys	Phe	Ala	Gly
								210	215						220
Pro	Tyr	Asp	Lys	Gly	Glu	Tyr	Ser	Pro	Ser	Val	Gln	Lys	Thr	Leu	Tyr
								225	230						240
Asp	Ile	Gln	Val	Leu	Thr	Leu	Gly	Gln	Val	Pro	Glu	Ile	Glu	Asp	Met
								245	250						255

Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys
 260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
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Tyr Gly Arg Ile Thr Gly Thr Val Lys Arg Lys Leu Thr Ser Arg Leu
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<210> 8

<211> 298

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PBC amino truncated

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 20 25 30

Ser Ile Lys Glu Val Ala Thr Ser Val Gln Leu Thr Leu Ser Ser Lys
 35 40 45

Lys Asp Tyr Leu His Gly Asp Asn Ser Asp Val Ile Pro Thr Asp Thr
 50 55 60

Ile Lys Asn Thr Val Asn Val Leu Ala Lys Phe Lys Gly Ile Lys Ser
 65 70 75 80

Ile Glu Thr Phe Ala Val Thr Ile Cys Glu His Phe Leu Ser Ser Phe
 85 90 95

Lys His Val Ile Arg Ala Gln Val Tyr Val Glu Glu Val Pro Trp Lys
 100 105 110

Arg Phe Glu Lys Asn Gly Val Lys His Val His Ala Phe Ile Tyr Thr
 115 120 125

Pro Thr Gly Thr His Phe Cys Glu Val Glu Gln Ile Arg Asn Gly Pro
 130 135 140

Pro Val Ile His Ser Gly Ile Lys Asp Leu Lys Val Leu Lys Thr Thr
 145 150 155 160

Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp Gln Phe Thr Thr Leu Pro
 165 170 175

Glu Val Lys Asp Arg Cys Phe Ala Thr Gln Val Tyr Cys Lys Trp Arg
 180 185 190

Tyr His Gln Gly Arg Asp Val Asp Phe Glu Ala Thr Trp Asp Thr Val
 195 200 205

Arg Ser Ile Val Leu Gln Lys Phe Ala Gly Pro Tyr Asp Lys Gly Glu
 210 215 220

Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr Asp Ile Gln Val Leu Ser
 225 230 235 240
 Leu Ser Arg Val Pro Glu Ile Glu Asp Met Glu Ile Ser Leu Pro Asn
 245 250 255
 Ile His Tyr Phe Asn Ile Asp Met Ser Lys Met Gly Leu Ile Asn Lys
 260 265 270
 Glu Glu Val Leu Leu Pro Leu Asp Asn Pro Tyr Gly Lys Ile Thr Gly
 275 280 285
 Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
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<210> 9

<211> 301

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PBC carboxy truncated

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Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
 20 25 30

Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
 35 40 45

Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
 50 55 60

Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
 65 70 75 80

Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
 85 90 95

His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
 100 105 110

Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
 115 120 125

His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
 130 135 140

Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
 145 150 155 160

Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
 165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
 180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
 195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
 210 215 220
 Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
 225 230 235 240
 Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met
 245 250 255
 Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys
 260 265 270
 Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
 275 280 285
 Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser
 290 295 300

<210> 10
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<400> 10
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 1 5 10 15
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 20 25 30
 Ser Ile Lys Glu Val Ala Thr Ser Val Gln Leu Thr Leu Ser Ser Lys
 35 40 45
 Lys Asp Tyr Leu His Gly Asp Asn Ser Asp Val Ile Pro Thr Asp Thr
 50 55 60
 Ile Lys Asn Thr Val Asn Val Leu Ala Lys Phe Lys Gly Ile Lys Ser
 65 70 75 80
 Ile Glu Thr Phe Ala Val Thr Ile Cys Glu His Phe Leu Ser Ser Phe
 85 90 95
 Lys His Val Ile Arg Ala Gln Val Tyr Val Glu Glu Val Pro Trp Lys
 100 105 110
 Arg Phe Glu Lys Asn Gly Val Lys His Val His Ala Phe Ile Tyr Thr
 115 120 125
 Pro Thr Gly Thr His Phe Cys Glu Val Glu Gln Ile Arg Asn Gly Pro
 130 135 140
 Pro Val Ile His Ser Gly Ile Lys Asp Leu Lys Val Leu Lys Thr Thr
 145 150 155 160
 Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp Gln Phe Thr Thr Leu Pro
 165 170 175
 Glu Val Lys Asp Arg Cys Phe Ala Thr Gln Val Tyr Cys Lys Trp Arg
 180 185 190

Tyr His Gln Gly Arg Asp Val Asp Phe Glu Ala Thr Trp Asp Thr Val
 195 200 205
 Arg Ser Ile Val Leu Gln Lys Phe Ala Gly Pro Tyr Asp Lys Gly Glu
 210 215 220
 Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr Asp Ile Gln Val Leu Thr
 225 230 235 240
 Leu Gly Gln Val Pro Glu Ile Glu Asp Met Glu Ile Ser Leu Pro Asn
 245 250 255
 Ile His Tyr Leu Asn Ile Asp Met Ser Lys Met Gly Leu Ile Asn Lys
 260 265 270
 Glu Glu Val Leu Leu Pro Leu Asp Asn Pro Tyr Gly Lys Ile Thr Gly
 275 280 285
 Thr Val Lys Arg Lys Leu Ser Ser Arg Leu
 290 295

<210> 11
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PKS carboxy truncated

<400> 11
 Met Ala His Tyr Arg Asn Asp Tyr Lys Lys Asn Asp Glu Val Glu Phe
 1 5 10 15
 Val Arg Thr Gly Tyr Gly Lys Asp Met Ile Lys Val Leu His Ile Gln
 20 25 30
 Arg Asp Gly Lys Tyr His Ser Ile Lys Glu Val Ala Thr Ser Val Gln
 35 40 45
 Leu Thr Leu Ser Ser Lys Lys Asp Tyr Leu His Gly Asp Asn Ser Asp
 50 55 60
 Val Ile Pro Thr Asp Thr Ile Lys Asn Thr Val Asn Val Leu Ala Lys
 65 70 75 80
 Phe Lys Gly Ile Lys Ser Ile Glu Thr Phe Ala Val Thr Ile Cys Glu
 85 90 95
 His Phe Leu Ser Ser Phe Lys His Val Ile Arg Ala Gln Val Tyr Val
 100 105 110
 Glu Glu Val Pro Trp Lys Arg Phe Glu Lys Asn Gly Val Lys His Val
 115 120 125
 His Ala Phe Ile Tyr Thr Pro Thr Gly Thr His Phe Cys Glu Val Glu
 130 135 140
 Gln Ile Arg Asn Gly Pro Pro Val Ile His Ser Gly Ile Lys Asp Leu
 145 150 155 160
 Lys Val Leu Lys Thr Thr Gln Ser Gly Phe Glu Gly Phe Ile Lys Asp
 165 170 175

Gln Phe Thr Thr Leu Pro Glu Val Lys Asp Arg Cys Phe Ala Thr Gln
180 185 190

Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu
195 200 205

Ala Thr Trp Asp Thr Val Arg Ser Ile Val Leu Gln Lys Phe Ala Gly
210 215 220

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr
225 230 235 240

Asp Ile Gln Val Leu Thr Leu Gly Gln Val Pro Glu Ile Glu Asp Met
245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Leu Asn Ile Asp Met Ser Lys
260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro
275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser
290 295 300

Serial No.: PCT/US99/17678
Applicant: Duke University
Title: PCT/US99/17678

Atty: BJS
Date: 11-19-99
Client:
Ref: 1579-379

Amendment
 Pages Specification
 Claims
 Sheets Drawings: Formal
 Informal
 Declaration (_____ Pages)
 Assignment
 Priority Document
 Base Issue Fee Transmittal
 Fee (Check)

Other: Sequence listing pages 37 - 49
disk (3.5")

